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RAW SEQUENCE LISTING DATE: 10/03/2002
PATENT APPLICATION: US/09/625,573 TIME: 14:00:12

Input Set : N:\CrF3\RULE60\09625573.raw
Output Set: N:\CRF4\10032002\I625573.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:
4 (i) APPLICANT: Charo, Israel
5 Coughlin, Shaun
6 (ii) TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
7 PROTEIN RECEPTORS
8 (iii) NUMBER OF SEQUENCES: 14
9 (iv) CORRESPONDENCE ADDRESS:
10 (A) ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
11 (B) STREET: 5 Palo Alto Square
12 (C) CITY: Palo Alto
13 (D) STATE: California
14 (E) COUNTRY: USA
15 (F) ZIP: 94306-2155
16 (v) COMPUTER READABLE FORM:
17 (A) MEDIUM TYPE: Floppy disk
18 (B) COMPUTER: IBM PC compatible
19 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
20 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
21 (vi) CURRENT APPLICATION DATA:
22 (A) APPLICATION NUMBER: US/09/625,573
23 (B) FILING DATE: 25-Jul-2000
24 (C) CLASSIFICATION:
25 (vii) PRIOR APPLICATION DATA:
26 (A) APPLICATION NUMBER: US/08/446,669
27 (B) FILING DATE: May 25, 1995
28 (viii) ATTORNEY/AGENT INFORMATION:
29 (A) NAME: Neeley, Richard
30 (B) REGISTRATION NUMBER: 30,092
31 (C) REFERENCE/DOCKET NUMBER: UCAL-237/01US
32 (ix) TELECOMMUNICATION INFORMATION:
33 (A) TELEPHONE: 415-843-5000
34 (B) TELEFAX: 415-857-0663
35 (C) TELEX: 380816CooleyPA
36 (2) INFORMATION FOR SEQ ID NO: 1:
37 (i) SEQUENCE CHARACTERISTICS:
38 (A) LENGTH: 2232 base pairs
39 (B) TYPE: nucleic acid
40 (C) STRANDEDNESS: single
41 (D) TOPOLOGY: linear
42 (ii) MOLECULE TYPE: cDNA
43 (iii) HYPOTHETICAL: NO
44 (iv) ANTI-SENSE: NO
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60 (ix) FEATURE:
62 (A) NAME/KEY: CDS
63 (B) LOCATION: 40..1161
65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
68 GGATTGAACA AGGACGCATT TCCCCAGTAC ATCCACAAAC ATG CTG TCC ACA TCT 54
69 Met Leu Ser Thr Ser
70 1 5
72 CGT TCT CGG TTT ATC AGA AAT ACC AAC GAG AGC GGT GAA GAA GTC ACC 102
73 Arg Ser Arg Phe Ile Arg Asn Thr Asn Glu Ser Gly Glu Glu Val Thr
74 10 15 20
76 ACC TTT TTT GAT TAT GAT TAC GGT GCT CCC TGT CAT AAA TTT GAC GTG 150
77 Thr Phe Phe Asp Tyr Asp Tyr Gly Ala Pro Cys His Lys Phe Asp Val
78 25 30 35
80 AAG CAA ATT GGG GCC CAA CTC CTG CCT CCG CTC TAC TCG CTG GTG TTC 198
81 Lys Gln Ile Gly Ala Gln Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe
82 40 45 50
84 ATC TTT GGT TTT GTG GGC AAC ATG CTG GTC GTC CTC ATC TTA ATA AAC 246
85 Ile Phe Gly Phe Val Gly Asn Met Leu Val Val Leu Ile Leu Ile Asn
86 55 60 65
88 TGC AAA AAG CTG AAG TGC TTG ACT GAC ATT TAC CTG CTC AAC CTG GCC 294
89 Cys Lys Lys Leu Lys Cys Leu Thr Asp Ile Tyr Leu Leu Asn Leu Ala
90 70 75 80 85
92 ATC TCT GAT CTG CTT TTT CTT ATT ACT CTC CCA TTG TGG GCT CAC TCT 342
93 Ile Ser Asp Leu Leu Phe Leu Ile Thr Leu Pro Leu Trp Ala His Ser
94 90 95 100
96 GCT GCA AAT GAG TGG GTC TTT GGG AAT GCA ATG TGC AAA TTA TTC ACA 390
97 Ala Ala Asn Glu Trp Val Phe Gly Asn Ala Met Cys Lys Leu Phe Thr
98 105 110 115
100 GGG CTG TAT CAC ATC GGT TAT TTT GGC GGA ATC TTC TTC ATC ATC CTC 438
101 Gly Leu Tyr His Ile Gly Tyr Phe Gly Ile Phe Phe Ile Ile Leu
102 120 125 130
104 CTG ACA ATC GAT AGA TAC CTG GCT ATT GTC CAT GCT GTG TTT GCT TTA 486
105 Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu
106 135 140 145
108 AAA GCC AGG ACG GTC ACC TTT GGG GTG GTG ACA AGT GTG ATC ACC TGG 534
109 Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr Ser Val Ile Thr Trp
110 150 155 160 165
112 TTG GTG GCT GTG TTT GCT TCT GTC CCA GGA ATC ATC TTT ACT AAA TGC 582
113 Leu Val Ala Val Phe Ala Ser Val Pro Gly Ile Ile Phe Thr Lys Cys
114 170 175 180
116 CAG AAA GAA GAT TCT GTT TAT GTC TGT GGC CCT TAT TTT CCA CGA GGA 630
117 Gln Lys Glu Asp Ser Val Tyr Val Cys Gly Pro Tyr Phe Pro Arg Gly
118 185 190 195
120 TGG AAT AAT TTC CAC ACA ATA ATG AGG AAC ATT TTG GGG CTG GTC CTG 678
121 Trp Asn Asn Phe His Thr Ile Met Arg Asn Ile Leu Gly Leu Val Leu
122 200 205 210
124 CCG CTG CTC ATC ATG GTC ATC TGC TAC TCG GGA ATC CTG AAA ACC CTG 726
125 Pro Leu Leu Ile Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu
126 215 220 225

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128	CTT CGG TGT CGA AAC GAG AAG AAG AGG CAT AGG GCA GTG AGA GTC ATC	774
129	Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Val Ile	
130	230 235 240 245	
132	TTC ACC ATC ATG ATT GTT TAC TTT CTC TTC TGG ACT CCC TAT AAC ATT	822
133	Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp Thr Pro Tyr Asn Ile	
134	250 255 260	
136	GTC ATT CTC CTG AAC ACC TTC CAG GAA TTC TTC GGC CTG AGT AAC TGT	870
137	Val Ile Leu Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Ser Asn Cys	
138	265 270 275	
140	GAA AGC ACC AGT CAA CTG GAC CAA GCC ACG CAG GTG ACA GAG ACT CTT	918
141	Glu Ser Thr Ser Gln Leu Asp Gln Ala Thr Gln Val Thr Glu Thr Leu	
142	280 285 290	
144	GGG ATG ACT CAC TGC TGC ATC AAT CCC ATC ATC TAT GCC TTC GTT GGG	966
145	Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly	
146	295 300 305	
148	GAG AAG TTC AGA AGC CTT TTT CAC ATA GCT CTT GGC TGT AGG ATT GCC	1014
149	Glu Lys Phe Arg Ser Leu Phe His Ile Ala Leu Gly Cys Arg Ile Ala	
150	310 315 320 325	
152	CCA CTC CAA AAA CCA GTG TGT GGA GGT CCA GGA GTG AGA CCA GGA AAG	1062
153	Pro Leu Gln Lys Pro Val Cys Gly Gly Pro Gly Val Arg Pro Gly Lys	
154	330 335 340	
156	AAT GTG AAA GTG ACT ACA CAA GGA CTC CTC GAT GGT CGT GGA AAA GGA	1110
157	Asn Val Lys Val Thr Thr Gln Gly Leu Leu Asp Gly Arg Gly Lys Gly	
158	345 350 355	
160	AAG TCA ATT GGC AGA GCC CCT GAA GCC AGT CTT CAG GAC AAA GAA GGA	1158
161	Lys Ser Ile Gly Arg Ala Pro Glu Ala Ser Leu Gln Asp Lys Glu Gly	
162	360 365 370	
164	GCC TAGAGACAGA AATGACAGAT CTCTGCTTTG GAAATCACAC GTCTGGCTTC	1211
165	Ala	
167	ACAGATGTGT GATTACAGT GTGAATCTTG GTGTCTACGT TACCAAGGCAG GAAGGCTGAG	1271
169	AGGAGAGAGA CTCCAGCTGG GTTGGAAAAC AGTATTTCC AAACCTACCTT CCAGTTCCTC	1331
171	ATTTTGAAAT ACAGGCATAG AGTCAGACT TTTTTAAAT AGTAAAATA AAATTAAAGC	1391
173	TGAAACTGC AACTTGTAAGA TGTGGTAAAG AGTTAGTTG AGTTGCTATC ATGTCAAACG	1451
175	TGAAATGCT GTATTAGTCA CAGAGATAAT TCTAGCTTTG AGCTTAAGAA TTTTGAGCAG	1511
177	TGGGTATGTT TGGGAGACTG CTGAGTCAAC CCAATAGTTG TTGATTGGCA GGAGTTGGAA	1571
179	GTGTGTGATC TGTGGCACA TTAGCCTATG TGCATGCAGC ATCTAAGTAA TGATGTCGTT	1631
181	TGAATCACAG TATACGCTCC ATCGCTGTC TCTCAGCTGG ATCTCCATTC TCTCAGGCTT	1691
183	GCTGCCAAAA GCCTTTGTTG TTTTGTGTTG TATCATTATG AAGTCATGCG TTTAATCACA	1751
185	TTCGAGTGT TCAAGTCTTC GCAGATGTC TTGATGCTCA TATTGTTCCC TAATTGCCA	1811
187	GTGGGAACTC CTAAATCAAAT TTGGCTTCTA ATCAAAGCTT TAAACCCCTA TTGGTAAAGA	1871
189	ATGGAAGGTG GAGAAGCTCC CTGAAGTAAG CAAAGACTTT CCTCTTAGTC GAGCCAAGTT	1931
191	AAGAATGTTT TTATGTTGCC CAGTGTGTTT CTGATCTGAT GCAAGCAAGA AACACTGGGC	1991
193	TTCTAGAACCTG AGGCAACTTG GGAACATAGAC TCCCAAGCTG GACTATGGCT CTACTTCAG	2051
195	GCCACATGGC TAAAGAAGGT TTCAGAAAGA AGTGGGGACA GAGCAGAACT TTCACCTTCA	2111
197	TATATTTGTA TGATCTTAAT GAATGCATAA AATGTTAAGT TGATGGTGAT GAAATGTAAA	2171
199	TACTGTTTT AACAACTATG ATTTGGAAAA TAAATCAATG CTATAACTAT GTTGATAAAA	2231
201	G	2232

204 (2) INFORMATION FOR SEQ ID NO: 2:
206 (i) SEQUENCE CHARACTERISTICS:

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PATENT APPLICATION: US/09/625,573

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Input Set : N:\Crf3\RULE60\09625573.raw
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207 (A) LENGTH: 374 amino acids
208 (B) TYPE: amino acid
209 (D) TOPOLOGY: linear
211 (ii) MOLECULE TYPE: protein
213 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
216 Met Leu Ser Thr Ser Arg Ser Arg Phe Ile Arg Asn Thr Asn Glu Ser
217 1 5 10 15
219 Gly Glu Glu Val Thr Thr Phe Phe Asp Tyr Asp Tyr Gly Ala Pro Cys
220 20 25 30
222 His Lys Phe Asp Val Lys Gln Ile Gly Ala Gln Leu Leu Pro Pro Leu
223 35 40 45
225 Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn Met Leu Val Val
226 50 55 60
228 Leu Ile Leu Ile Asn Cys Lys Lys Leu Lys Cys Leu Thr Asp Ile Tyr
229 65 70 75 80
231 Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu Phe Leu Ile Thr Leu Pro
232 85 90 95
234 Leu Trp Ala His Ser Ala Ala Asn Glu Trp Val Phe Gly Asn Ala Met
235 100 105 110
237 Cys Lys Leu Phe Thr Gly Leu Tyr His Ile Gly Tyr Phe Gly Gly Ile
238 115 120 125
240 Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His
241 130 135 140
243 Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr
244 145 150 155 160
246 Ser Val Ile Thr Trp Leu Val Ala Val Phe Ala Ser Val Pro Gly Ile
247 165 170 175
249 Ile Phe Thr Lys Cys Gln Lys Glu Asp Ser Val Tyr Val Cys Gly Pro
250 180 185 190
252 Tyr Phe Pro Arg Gly Trp Asn Asn Phe His Thr Ile Met Arg Asn Ile
253 195 200 205
255 Leu Gly Leu Val Leu Pro Leu Leu Ile Met Val Ile Cys Tyr Ser Gly
256 210 215 220
258 Ile Leu Lys Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg
259 225 230 235 240
261 Ala Val Arg Val Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp
262 245 250 255
264 Thr Pro Tyr Asn Ile Val Ile Leu Leu Asn Thr Phe Gln Glu Phe Phe
265 260 265 270
267 Gly Leu Ser Asn Cys Glu Ser Thr Ser Gln Leu Asp Gln Ala Thr Gln
268 275 280 285
270 Val Thr Glu Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile
271 290 295 300
273 Tyr Ala Phe Val Gly Glu Lys Phe Arg Ser Leu Phe His Ile Ala Leu
274 305 310 315 320
276 Gly Cys Arg Ile Ala Pro Leu Gln Lys Pro Val Cys Gly Gly Pro Gly
277 325 330 335
279 Val Arg Pro Gly Lys Asn Val Lys Val Thr Thr Gln Gly Leu Leu Asp
280 340 345 350

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282 Gly Arg Gly Lys Gly Lys Ser Ile Gly Arg Ala Pro Glu Ala Ser Leu
283 355 360 365

285 Gln Asp Lys Glu Gly Ala
286 370

289 (2) INFORMATION FOR SEQ ID NO: 3:

291 (i) SEQUENCE CHARACTERISTICS:

292 (A) LENGTH: 1979 base pairs
293 (B) TYPE: nucleic acid
294 (C) STRANDEDNESS: single
295 (D) TOPOLOGY: linear

297 (ii) MOLECULE TYPE: cDNA

299 (iii) HYPOTHETICAL: NO

301 (iv) ANTI-SENSE: NO

303 (ix) FEATURE:

304 (A) NAME/KEY: CDS

305 (B) LOCATION: 81..1160

307 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

310 CAGGACTGCC TGAGACAAGC CACAAGCTGA ACAGAGAAAG TGGATTGAAC AAGGACGCAT 60

312 TTCCCCAGTA CATCCACAAC ATG CTG TCC ACA TCT CGT TCT CGG TTT ATC 110

313 Met Leu Ser Thr Ser Arg Ser Arg Phe Ile
314 1 5 10

316 AGA AAT ACC AAC GAG AGC GGT GAA GAA GTC ACC ACC TTT TTT GAT TAT 158

317 Arg Asn Thr Asn Glu Ser Gly Glu Glu Val Thr Thr Phe Phe Asp Tyr

318 15 20 25

320 GAT TAC GGT GCT CCC TGT CAT AAA TTT GAC GTG AAG CAA ATT GGG GCC 206

321 Asp Tyr Gly Ala Pro Cys His Lys Phe Asp Val Lys Gln Ile Gly Ala

322 30 35 40

324 CAA CTC CTG CCT CCG CTC TAC TCG CTG GTG TTC ATC TTT GGT TTT GTG 254

325 Gln Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val

326 45 50 55

328 GGC AAC ATG CTG GTC CTC ATC TTA ATA AAC TGC AAA AAG CTG AAG 302

329 Gly Asn Met Leu Val Val Leu Ile Leu Ile Asn Cys Lys Lys Leu Lys

330 60 65 70

332 TGC TTG ACT GAC ATT TAC CTG CTC AAC CTG GCC ATC TCT GAT CTG CTT 350

333 Cys Leu Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu

334 75 80 85 90

336 TTT CTT ATT ACT CTC CCA TTG TGG GCT CAC TCT GCT GCA AAT GAG TGG

337 Phe Leu Ile Thr Leu Pro Leu Trp Ala His Ser Ala Ala Asn Glu Trp

338 95 100 105

340 GTC TTT GGG AAT GCA ATG TGC AAA TTA TTC ACA GGG CTG TAT CAC ATC 446

341 Val Phe Gly Asn Ala Met Cys Lys Leu Phe Thr Gly Leu Tyr His Ile

342 110 115 120

344 GGT TAT TTT GGC GGA ATC TTC TTC ATC ATC CTC CTG ACA ATC GAT AGA 494

345 Gly Tyr Phe Gly Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg

346 125 130 135

348 TAC CTG GCT ATT GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACG GTC 542

349 Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val

350 140 145 150

352 ACC TTT GGG GTG GTG ACA AGT GTG ATC ACC TGG TTG GTG GCT GTG TTT 590

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/625,573

DATE: 10/03/2002

TIME: 14:00:13

Input Set : N:\Crf3\RULE60\09625573.raw
Output Set: N:\CRF4\10032002\I625573.raw

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:856 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=9
L:874 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=10